



8. (Withdrawn) A method for identifying a compound that is useful in treating a neuropsychiatric or neurodevelopmental disorder, which method comprises detecting modulation of of PAMP expression in a transgenic animal that expresses PAMP, wherein the animal is contacted with the compound.
9. (Withdrawn) The method of claim 8, wherein the disorder is schizophrenia.
10. (Previously Presented) A method for identifying a candidate compound for treating a neuropsychiatric or neurodevelopmental disorder, which method comprises:
  - (a) contacting a reconstituted system for measuring presenilin associated membrane protein (PAMP) activity, comprising a PAMP, or a functional fragment thereof, and a PAMP substrate, with a test compound, the PAMP comprising an amino acid sequence at least 90% identical to at least one amino acid sequence selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16 and SEQ ID NO:18; and
  - (b) detecting a difference in PAMP activity in the presence of the compound compared to PAMP activity in the absence of the compound,wherein the difference in PAMP activity identifies the candidate compound.
11. (Original) The method of claim 10, wherein the disorder is schizophrenia.



18. (Previously Presented) The method of claim 10, wherein the PAMP substrate is presenilin 1.
19. (Previously Presented) The method of claim 10, wherein the PAMP substrate is  $\beta$ APP.
20. (Previously Presented) The method of claim 10, wherein the PAMP amino acid sequence comprises at least one amino acid sequence motif starting at a position corresponding to a residue of SEQ ID NO:14 selected from the group consisting of NKTA at residue 45, NATH at residue 55, NETK at residue 187, NGSA at residue 204, NQSQ at residue 417, NISG at residue 435, NNSW at residue 530, NTTY at residue 562, NLTG at residue 573, NLTR at residue 580, SGAG at residue 404, GCQSSI at residue 61, GNGLAY at residue 167, GAESAV at residue 294, GVV LAD at residue 438, TSR at residue 115, SSR at residue 340, SQK at residue 384, TRLD at residue 280, SFVE at residue 361, SIYD at residue 455, SSTE at residue 641, and combinations thereof.
21. (Previously Presented) The method of claim 20, wherein the PAMP amino acid sequence comprises the amino acid sequence motifs, starting at positions corresponding to residues of SEQ ID NO:14, NKTA at residue 45, NATH at residue 55, NETK at residue 187, NGSA at residue 204, NQSQ at residue 417, NISG at residue 435, NNSW at residue 530, NTTY at residue 562, NLTG at residue 573, NLTR at residue 580, SGAG at residue 404, GCQSSI at residue 61, GNGLAY at residue 167, GAESAV at residue 294, GVV LAD at residue 438, TSR at residue 115, SSR at residue 340, SQK at residue 384, TRLD at residue 280, SFVE at residue 361, SIYD at residue 455, and SSTE at residue 641.

22. (Previously Presented) The method of claim 21, wherein the PAMP has the amino acid sequence of SEQ ID NO:16.
23. (Previously Presented) The method of claim 21, wherein the PAMP has the amino acid sequence of SEQ ID NO:14.